

<110> TAISEI CORPORATION

<110> AJINOMOTO CO., INC.

<120> GENE THAT IMPARTS SALT STRESS TOLERANCE

<130> PH-2125-PCT

<150> JP2003-113194

<151> 2003-04-17

<150> JP2004-075932

<151> 2004-03-17

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1554

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (131)..(1222)

<400> 1

ggcacgagga gcgccgccgc cggttgccag aactgccag tgcaacagag ccgcaaaacc 60

acacgcccc tcgcgcgtc acacagagag agacacacag atcgatcgag cggccggccg 120

gacggcgcag atg gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg 169

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala

1

5

10

ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc 217

Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile

15

20

25

ggc acg cac acg gcg ctg cgc ctg ctg gag cag ggc tac ggc gtc acc 265

Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr

30

35

40

45

gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc 313

Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val

50

55

60

cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cgg 361

Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg

65

70

75

ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg 409

Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg

80

85

90

agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag 457

Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu

95

100

105

agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc 505

Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr

110

115

120

125

atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg 553

Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val

130

135

140

ttc tgc tgc tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc 601

Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys

145

150

155

gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag 649

Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys

160

165

170

ctc atc ctg gag gag ttg gcg cgg gac tac cag cgc gcg gac ccg ggc 697

Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly

175

180

185

tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc 745

Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser

190

195

200

205

tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg 793

Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu

210

215

220

ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc 841

Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val

225

230

235

tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac 889

Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr

240

245

250

ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag 937

Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys

255

260

265

ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca 985

Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr

270

275

280

285

ggg cgc ggc aca tcc gtt ctc gag atg gtg gcg gcg ttc aag aag gca 1033

Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala

290

295

300

tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac 1081

Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp

305

310

315

gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctc gga 1129

Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly

320

325

330

tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac 1177

Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn

335

340

345

tgg gcc aag aag aac ccc tat ggc tac tgc ggc act gcc gaa aaa 1222

Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys

350

355

360

tagagcgcgt gcattaatca gatctctgga ctgaatttgt ccatggttga tggttgtctc 1282

agacctatcg gtggaagatg taacaagtag agaccgctcg aatgtgccta gctacgaaag 1342

tttcgtacca tctctcttgt cataacctca tgtagatggt cattttattg gaattagcct 1402

tagccttcag gcccggcgct gttagccatt gcttgctatc gaggtagggt gggttggaac 1462

tttgggcgcc cttgaacttc cattatcatc attgcacag acggcacagt tgcgcagtga 1522

gccgttgact gcttgtgaaa aaaaaaaaaa aa 1554

<210> 2

<211> 364

<212> PRT

<213> Seashore Paspalum

<400> 2

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala Gly Ala Ser

1

5

10

15

Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr His

20

25

30

Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp

35

40

45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile

50

55

60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu

65

70

75

80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp

85

90

95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala

100

105

110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu

115

120

125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser

130

135

140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp  
145 150 155 160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu  
165 170 175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile  
180 185 190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu  
195 200 205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile  
210 215 220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His  
225 230 235 240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val  
245 250 255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp  
260 265 270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly  
275 280 285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys  
7/21

290

295

300

Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu

305

310

315

320

Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala

325

330

335

Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys

340

345

350

Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys

355

360

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 3

ggtgcgacg actcctggag cccg

24

<210> 4

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 4

ttgacaccag accaactggt aatg

24

<210> 5

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 5

tgccgtgggc tccggcgggt tcgccttcca cgagcaccac gagaagaagg aggaccacaa 60  
ggacgccgag gaggccggcg gcgagaagaa gcaccacttc ttcggctgat ccatctcacc 120  
atctccatct cccacccccca tcgatccatt tgtgttggct ttaattccct gcgtgcatgc 180  
gtgttgttga ataaggggcc ggttccatct gtacgtacgt gtactccgag acctatcgtc 240  
atgtgtgtgt gtgtacgtat acctgctgtg tacatgatgg tcgtatatgc cactggacta 300  
tgtgtgtgtg caactctgtt ctgatttgct atatataag 339

<210> 6

<211> 497

<212> DNA

<213> Seashore Paspalum

<400> 6

tgcagggacc agtgggaactg ggccaagaag aaccctatg gctactgcgg cactgccgaa 60  
aaatagagcg cgtgcattaa tcagatctct ggactgaatt tgtccatggt tgatggttgt 120  
ctcagaccta tcgggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180  
agtttcgtac catctctctt gtcataacct catgtagatg gtcattttat tggaattagc 240  
cttagccttc aggcccggcg ctgttaaaat ttgttttaca catggatttt ctcgctacgt 300  
gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca 360  
cgacggtggc tacgccctgt gttgtagtac tgtgaatatg atgtggtaat aacaataact 420  
tgcagtgaga cttcagcttt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480  
aaaaaaaaaa aaaaaaa 497

<210> 7

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 7

ggccgctgtg cagggaccag tggaactggg ccaagaagaa cccctatggc tactgcggca 60  
ctgccgaaaa atagagcgcg tgcattaatc agatctcttg actgaatttg tccatggttg 120  
atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct 180  
agctacgaag tttcgtacca tctctcttgt cataacctca tgtagatggt catttttattg 240  
gaattagcct tagccttcag gcccggcgct gttaaaatit gttttacaca tggattttct 300  
cgctacgtgt gatacatatt gtgtctgtaa taatcctgat cggagtttcc agtaataaaa 360  
ccgateccag acggtggcta cgccctgtgt tgtagt 396

<210> 8

<211> 1540

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (110)..(1183)

<400> 8

ggcacgaggg agagattgag aggaaatcga gttcatcctc cctccaccat cgccgatcat 60

agccttcctt tccccgatcg ccgatccgat ccacaagcaa gcagccagg atg gtt tct 118

Met Val Ser

1

gcg gtg ctt cgt acc atc ctt gtg acg ggc ggc gcc ggc tac atc ggc 166

Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly

5

10

15

agc cac acc gtg ctg ctg ctg ctg cag cag gga ttc cgc gtc gtc gtc 214

Ser His Thr Val Leu Leu Leu Leu Gln Gln Gly Phe Arg Val Val Val

20

25

30

35

gtc gac aac ctc gac aac gcc tcc gac gtc gcg ctc gcc cgc gtc gcg 262

Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala Arg Val Ala

40

45

50

cag ctc gca gca agc agc aac ggc ggc gcc gcc aac ctc gtc ttc cac 310

Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu Val Phe His

55

60

65

aag gtt gac ctt cgc gac agg cac gcg ctg gag gac atc ttc tcc tcc 358

Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile Phe Ser Ser

70

75

80

cac agg ttt gag gct gtg att cat ttt gct ggg ctc aaa gct gtt ggc 406

His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly

85

90

95

gag agc gtg cag aag ccg ctg ctt tac tac gac aac aac ctc atc ggc 454

Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly

100

105

110

115

acc atc acc ctc ctc gag gtc atg gcc gca cat ggc tgc aag aag ctg 502

Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu

120

125

130

gtg ttc tcg tca tct gca act gtc tat ggg tgg ccc aag gaa gtg cca 550

Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro

135

140

145

tgc acc gaa gaa ttc cct ctt tgc gcc acc aac ccc tat ggg cga acc 598

Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr Gly Arg Thr

150

155

160

aag ctt gtg att gaa gat atc tgc cgc gac gtc cac cgt tca gac cct 646

Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg Ser Asp Pro

165

170

175

gat tgg aag atc ata ctg ctc agg tac ttc aac cct gtt ggt gct cat 694

Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His

180

185

190

195

cca agc gga cac atc ggt gaa gac ccc tct gga atc cca aac aac ctg 742

Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu

200

205

210

atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg cct cac ctc act 790

Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr

215

220

225

gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat 838

Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp

230

235

240

tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg 886

Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly

245

250

255

aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg 934

Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu

260

265

270

275

ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag 982

Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu

280

285

290

aag gtt tct ggc aag aaa atc cct ctg gtg ctt gct ggg cga aga cct 1030

Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro

295

300

305

gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag 1078

Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu

310

315

320

ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag 1126

Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln

325

330

335

tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac 1174

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp

340

345

350

355

aac agc agc tgactgaaag caaatgcatg ctatgcatga tagggagatc 1223

Asn Ser Ser

gagcagcaga ccacttacca ctgctagtaa aagaagtcga gtctcagaat accaccgtac 1283

gtatgcttac taaatagtcc gaggacggac ggacggatga tccatgtgtg gggcctcgta 1343

ttctcatttg tatagagga cggagtagga gatccccagt cccatccatc cggtttattg 1403

ttgctaccgt caatccatgt ttaagaaata aaccctatg catgtatgct tatcgatcta 1463

ctgtactagc taattatata ggcatatgta tatttgtag attcttatac aaaaaaaaaa 1523

aaaaaaaaaa aaaaaaa 1540

<210> 9

<211> 358

<212> PRT

<213> Seashore Paspalum

<400> 9

Met Val Ser Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly

1 5 10 15

Tyr Ile Gly Ser His Thr Val Leu Leu Leu Leu Gln Gln Gly Phe Arg

20 25 30

Val Val Val Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala

35 40 45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu

50 55 60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile

65	70	75	80
Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys			
	85	90	95
Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn			
	100	105	110
Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys			
	115	120	125
Lys Lys Leu Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys			
	130	135	140
Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr			
145	150	155	160
Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg			
	165	170	175
Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val			
	180	185	190
Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro			
	195	200	205
Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro			
	210	215	220



His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly

225 230 235 240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala

245 250 255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val

260 265 270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala

275 280 285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly

290 295 300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala

305 310 315 320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys

325 330 335

Arg Asp Gln Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly

340 345 350

Ser Pro Asp Asn Ser Ser

355

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 10

acagagccgc aaaaccacac

20

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 11

ttcgtagcta ggcacattcg agcgggtg

27

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 12

gtcgtcgaca acttccacaa

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 13

ttgttctcg tagtacatgtc

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 14

atgaaaaagc ctgaactcac

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 15

cgaacccgct cgtctggcta

20

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 16

gtggtcgaca acttcacaa

20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 17

ttgttctcgt acatgta

17